IN THE SPECIFICATION:

Please amend the title as follows:

[[A]] Molecular ~~Marker~~ Markers of Plant Embryogenesis

Please amend the paragraph beginning on page 12, line 1 as follows:

Figure 3 is the nucleotide (SEQ ID NO: 3) and deduced amino acid (SEQ ID NO: 2) sequences of OPEm1.

Please amend the paragraph beginning on page 12, line 18 as follows:

Figure 5 is the sequence alignment of OPEm1 (SEQ ID NO: 2) with examples of 1-Cys and 2-Cys peroxiredoxins. The '*' denotes a single fully conserved residue. The ':' denotes conservation of strong groups. The '.' conservation of weak groups. Those without any symbol denote no consensus (CLUSTALW), Biology Workbench Version 3.2, University of Illinois, 1999). The amino acid sequences were obtained from Genbank: HvPer1 (*Hordeum vulgare*, barley, P52572) (SEQ ID NO: 7), AtPer1 (*Arabidopsis thaliana*, thalecress, CAA63909) (SEQ ID NO: 8) and C2CPRX (*Brassica campestris* L. ssp. *pekinensis*, chinese cabbage) (SEQ ID NO: 9).

Please amend the paragraph beginning on page 12, line 26 as follows:

Figure 6 is the sequence alignment of OPEm1 (SEQ ID NO: 2) with examples of other members of 1-Cys peroxiredoxin. The '*' denotes a single fully conserved residue. The ':' denotes conservation of strong groups. The '.' denotes conservation of weak groups. Those without any symbols denote no consensus. (CLUSTALW, Biology Workbench Version 3.2, University of Illinois, 1999). The peroxiredoxin amino acid sequences were obtained from Genebank: HvPer1 (*Hordeum vulgare*, barley, P52572) (SEQ ID NO: 7) and AtPer1 (*Arabidopsis thaliana*, thalecress, CAA63909) (SEQ ID NO: 8). The '#' and '@' denote the positively charged residue

His 38 and Arg 128 respectively, which are all found close to the Cys 46. The PVCT region represents a specific characteristic of the 1-Cys peroxiredoxin. The basis residues at the terminal end of the 1-Cys peroxiredoxin align to the nuclear localization signal (NLS) region that is not present in OPEm1. A coloured version of this Figure where the PVCT region is in blue and the basic region is in red is available from the Applicant upon request.

Please amend the paragraph beginning on page 46, line 10 as follows:

Clones to be sequenced were sent to ACGT (USA) and the sequencing was performed on a single-run basis using universal primers T3/T7 for most clones except for clones from the enriched library, where the primers PN1/PN2 were used. Sequence analyses were carried out using DNASIS (Hitachi software package, 1997) and BLAST (Basic Local Alignment Search Tool) (Altshul *et al.*, 1990; 1997), available *via* the internet at http://www.ncbi.nlm.nih.gov. To analyze the sequences wit their closely related counterparts, the alignment of the sequences was done using the CLUSTALW programme available from the Biology Workbench version 3.2 on line ~~at http://biology.ncsa.uiuc.edu~~.